Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1 (Currently Amended). A screening method for simultaneous detection of diarrheagenic *Shigella* species and *E. coli* (DEC) including A/EEC & EPEC, ETEC, VTEC, EIEC and strains with the *ehxA* gene, wherein said method comprises

performing multiplex PCR with two or more primers in a single reaction, wherein the primers comprise at least one primer which specifically amplifies *exhA*, at least a second primer selected from a primer which specifically amplifies *vtx1* or a primer which specifically amplifies *vtx2*, and at least one primer which specifically amplifies a further gene selected from the group consisting of *ipaH, eae, sta* or *estA, vtx1, vtx2* and *elt*, at least one of the primers being selected from Table 3; and

identifying subjects having amplified *exhA and vtx1* or *vtx2* genes.

~~a) detecting *Shigella* species by detecting the presence of the *ipaH* gene;~~

~~b) incorporation of a 16S rDNA positive control;~~

~~c) primers chosen to match all clinically relevant subtypes of the given virulence gene;~~

~~d) performance with multiplex PCR;~~

~~e) a PCR setup designed to enclose all primer sets in one single reaction, leading to the specific amplification of any given template present;~~

~~f) primers selected from table 3;~~

~~g) use of the UNG system~~.

Claims 2 – 38 (Canceled).

39 (Currently Amended). The screening method according to claim 1, further comprising amplifying and detecting the genes ~~selected from the group~~ comprising: *ipaH, eae, sta, vtx1, vtx2,* and *elt,* parts of these genes or products of these genes or parts thereof, such as RNA or polypeptides.

40 (Currently Amended). The screening method according to claim 1, further comprising detecting the genes ~~selected from the group~~ comprising: *ipaH, eae, ehxA, sta, vtx1, vtx2, elt,* and *bfpA,* parts of these genes or products of these genes or parts thereof, such as RNA or polypeptides.

41 (Previously Presented). The screening method according to claim 1 wherein the genes are detected by size identification.

42 (Previously Presented). The screening method according to claim 41 wherein the means for detecting by size identification is performed by agarose gel electrophoresis or capillary electrophoresis.

43 (Currently Amended). The screening method according to claim 1 wherein the genes are detected with a hybridization probe for each of the amplified genes.

44 (Previously Presented). The screening method according to claim 43 wherein the probes are selected from table 7.

45 (Previously Presented). The screening method according to claim 1 wherein the material to be analyzed is selected from the group consisting of stool samples, consumables, bacterial cultures, and sewage samples.

46 (Previously Presented). The screening method according to claim 45, in which the testing is carried out on a sample from a human or an animal or from food or beverages.

47 (Currently Amended). The screening method according to claim 1, in which the primers selected for the multiplex PCR further comprise a primer having a ~~used are selected from the group consisting of~~:

~~a) the primers of table 3;~~

~~b)~~ sequences having a sequence identity of at least 80% (such as at least 85%, at least 90%, or at least 95%) with the primer sequences of table 3 ~~a)~~;

~~c)~~ parts of the sequences in table 3 ~~a) or b),~~ having a length of more than 10, preferably more than 13 nucleotides; and

~~d)~~ sequences comprising a sequence in table 3 ~~a), b) or c), said sequence~~ having a length of no more than 100 nucleotides.

48 (Currently Amended). The screening method according to claim 47 wherein said primers consist of 14, 15, 16, 17, 18, 19, 20, 21 or 22 consecutive nucleotides ~~of the sequences in a) or b)~~.

49 (Currently Amended). The screening method according to claim 47 wherein said primers consist of at most 90, 80, 70, 60, 50, 40, or 30 nucleotides ~~of the sequences comprising a), b), or c)~~.

50 (Currently Amended). The screening method according to claim 43 ~~1~~, in which the sequences are detected using two or more probes ~~used are~~ selected from the group consisting of:

~~a)~~ the probe sequences of table 7;

b) sequences having a sequence identity of at least 80% with the primer sequences of a);

c) parts of the sequences in a) or b), having a length of more than 10, preferable more than 16 nucleotides, such as more than 17, 18, 19 or 20 nucleotides;

d) sequences comprising a sequence in a), b) or c), said sequence having a length of no more than 100 nucleotides.

51 (Previously Presented). The screening method according to claim 50 wherein said probes have at least 85%, 90%, or 95% sequence identity with the sequences of a).

52 (Previously Presented). The screening method according to claim 50 wherein said probes consist of 14, 15, 16, 17, 18, 19, 20, 21 or 22 consecutive nucleotides of the sequences in a) or b).

53 (Previously Presented). The screening method according to claim 50 wherein said probe consist of at most 90, 80, 70, 60, 50, 40, or 30 nucleotides of the sequences comprising a), b), or c).

54 (Previously Presented). A kit which comprises, in a single or in separate containers, nucleotide sequences which are able to prime amplify, in a nucleotide sequence amplification reaction, the genes: *ipaH, eae, sta, vtx1, vtx2,* and *elt* or parts of these genes or the complementary strands to the genes or parts thereof and which comprises a control.

55 (Previously Presented). The kit according to claim 54 wherein the sequence amplification reaction is PCR.

56 (Previously Presented). The kit according to claim 54 wherein the control consists of primers for 16s rDNA.

57 (Previously Presented). The kit according to claim 54 wherein the nucleotide sequences for priming are selected from the group consisting of the priming sequences in table 3.

58 (Previously Presented). The kit according to claim 54 wherein the nucleotide sequences for probing are selected from the group consisting of the probe sequences in table 7.

59 (Previously Presented). The kit according to claim 54 which comprises a means for detecting by size identification.

60 (Previously Presented). The kit according to claim 59 wherein the means for detecting by size identification is performed by agarose gel electrophoresis or capillary electrophoresis.